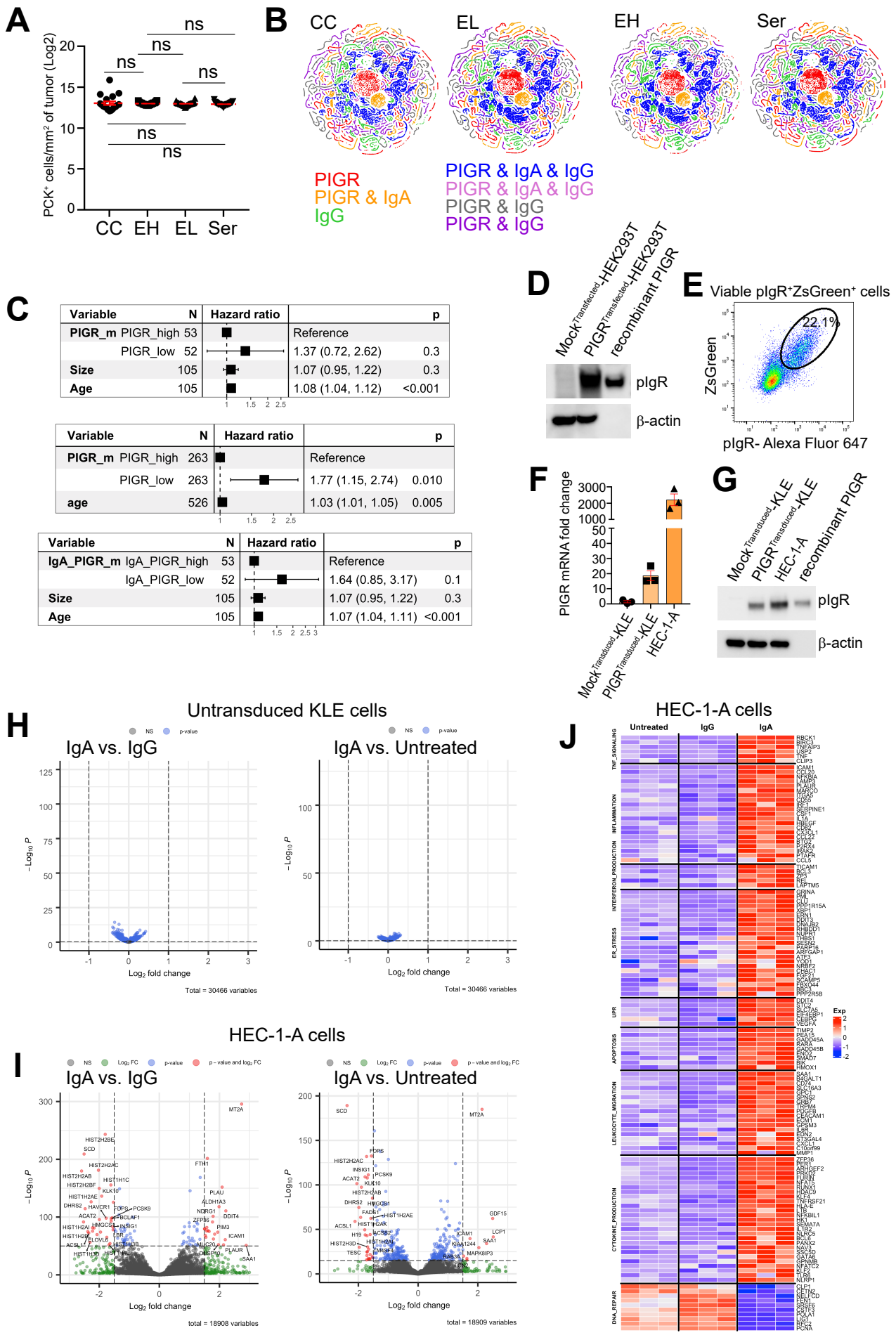
Supplementary Figure S3



Supplementary Figure S3. pIgR expression is necessary for non-antigen-specific IgA-mediated transcriptional changes. (**A**) PCK^+ densities across histology types, calculated using the number of PCK^+ cells among total cells and further normalized with unit area (mm^2), and averaged from duplicated cores. ns, not significant, $P > 0.05$. Unpaired two-tailed Mann Whitney test. (**B**) t-SNE embedding of 90 thousand tumor cells highlighting diverse antibody clusters across the four histology types. Each dot is a cell and colors correspond to cell types inferred by spatial neighborhood-based clustering. Unique spatial neighborhoods are characterized by spatially-distinct clusters. Certain clusters with the same name are differently colored because they are spatially distinct clusters. Each cell represents not only itself but also its immediate neighborhood and this is used for identifying spatial clusters or 'cellular neighborhoods'. A sample can be viewed as a collection of such cellular neighborhoods where the same functional cluster can exist in multiple spatial locations. CC, clear cell endometrial cancer; EH, endometrioid type high grade (grade 3) endometrial cancer; EL, endometrioid type low grade endometrial cancer; Ser, Serous endometrial cancer. (**C**) Multivariable Cox regression analysis showing tumor size or patient's age adjusted Hazard ratios and *P* values, which are corresponding to the Kaplan-Meier plots shown in **Fig.1E-G.** (**D**) Western blot confirming pIgR overexpression in HEC-293T cells, used for lentivirus production, compared to $mock^{transfected}$ cells. Recombinant human pIgR was used as a positive control. β-actin was used as loading control. (**E**) FACS dot plot showing the sorting of gated $ZsGreen^+pIgR^+$ cells from lentivirally transduced KLE cells. (**F**) Q-RT PCR showing *PIGR* mRNA fold changes in $mock^{transduced}$, $PIGR^{transduced}$, and HEC-1-A cells. (**G**) Western blots showing pIgR levels in $mock^{transduced}$, $PIGR^{transduced}$, and HEC-1-A cells. Recombinant human pIgR was used as a positive control. β-actin was used as loading control. (**H**) Volcano plots showing differential analysis results for comparisons between IgA- and IgG-treated (*left*) or between IgA-

treated and untreated (*right*) untransduced KLE cells. The cutoff for significance is FDR adjusted p-value <0.05 and log2FC>1 or log2FC< -1. (**I**) Volcano plots showing differential analysis results for comparisons between IgA- and IgG-treated (*left*) or between IgA-treated and untreated (*right*) HEC-1-A cells. The cutoff for significance is FDR adjusted p-value <0.05 and log2FC>1 or log2FC< -1. (**J**) Pre-ranked gene-set enrichment analysis (GSEA), showing the top upregulated gene sets in HEC-1-A cells treated with irrelevant IgA compared to IgG or untreated cells (n = 3), Kolmogorov–Smirnov test.